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Paternity Test Through Kinship Analysis as Forensic Identification Technique

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Abstract

Paternity tests is often faced with the unavailability of information from the father, mother, or child as a comparison in forensic DNA examination process. Therefore, comparisons with information from close family lines are needed, for example from the victim's siblings or the perpetrator if there are no comparisons from parents or siblings. This study was conducted by the Human Genetic Study Group of Airlangga University in its campus from January to April 2020. The aim of the study was to analyze the use of kinship analysis in paternity test through STR CODIS examination on siblings. This was an observational laboratory study with a temporary design. DNA sample extraction level and purity results were measured with the mean DNA sample level of 675±5.35ng/μL, while the purity values ranged from 1.05 to 1.86. The paternity test principle is based on comparison process between the parents' alleles with the child's alleles. However, if the parents' alleles are not available, the siblings' alleles can be used as a comparison for identification purpose, which is known as kinship analysis. Statistically, full siblings have a 2 alleles accuracy probability of [0.25] 25%, which was the same as not having the same allele or 0 allele, while 1 allele accuracy reached 50%. All CODIS STR loci had the highest percentage of 2 allele sharing. Therefore, it is recommended to use sibling or kinship analysis if both parents are absent.

Keywords: Kinship analysis, paternity test, sibling, STR CODIS

Tes Keayahan Melalui Analisis Hubungan Kekerabatan Saudara sebagai Teknik Identifikasi Forensik

Abstrak

Tes paternitas seringkali dihadapkan tidak tersedianya informasi pihak ayah, ibu atau anak dijadikan sebagai pembanding dalam proses pemeriksaan DNA forensik. Oleh karena itu diperlukan perbandingan dengan informasi dari garis keluarga dekat, misalnya dari saudara korban atau pelaku jika tidak ada pembanding dari orang tua atau saudara kandung. Penelitian dilakukan di Kelompok Studi Genetik Manusia Universitas Airlangga pada bulan Januari sampai April tahun 2020. Penelitian ini bertujuan menganalisis kinship dalam tes paternitas melalui pemeriksaan STR CODIS pada saudara kandung. Penelitian merupakan penelitian laboratorium observasional dengan desain sementara. Tingkat ekstraksi sampel DNA dan hasil kemurnian diukur, dengan tingkat sampel DNA rata-rata 675±5.35ng/μL, sedangkan nilai kemurnian berkisar 1.05–1.86. Prinsip uji garis ayah didasarkan pada proses perbandingan antara alel orang tua dengan alel anak. Namun jika alel orang tua tidak tersedia, maka alel saudara kandung dapat digunakan sebagai pembanding sebagai metode identifikasi yang disebut dengan analisis kinship. Secara statistik full sibling memiliki probabilitas akurasi 2 alel sebesar [0.25] 25%, nilai ini sama dengan tidak memiliki alel atau 0 alel yang sama, sedangkan akurasi 1 alel mencapai 50%. Semua lokus CODIS STR memiliki persentase tertinggi dari 2 pembagian alel. Oleh karena itu disarankan untuk menggunakan analisis saudara kandung atau kekerabatan jika kedua orang tua tidak ada.

Kata kunci: Analisis kinship, keluarga, STR CODIS, tes paternitas

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Introduction

Individual forensic identification, especially a paternity test (paternity test), is often faced with unavailable information from the parents or the children that can be used as a comparison in forensic deoxyribonucleid acid [DNA] examination process. Forensic DNA examination principle is based on allele comparison from the victim or the perpetrator that will be compared to allele from the family or kinship lines (kinship analysis) for example in cases of "unborn child disputed", paternity disputed or even on forensic DNA analysis in mass disaster as well as war victims. In this condition, comparison from close family lines are needed as one of alternatives in forensic DNA analysis process, for example DNA from the siblings of the victims or the perpetrators if comparisons from the parents or the children are not available.[1]

Paternity test is a tool to determine whether a man is the biological father of someone. Paternity test is a legal procedure for fatherhood. To determine paternity itself is difficult because there are many things to prove. Currently, to solve the problem of paternity it starts with similarity aspect or from the point of view that there is no similarity between the child and the alleged father. The similarities referred to are the characteristics of eye and hair color, distinct way of behaving or speaking, and height.[2]

Unavailable information from both parents as a comparison in identification examination process is one of problems that might occur in forensic DNA analysis, especially in paternity test. Therefore, a comparison is needed from a close family or kinship line as one of alternatives that might be considered in forensic DNA analysis process, such as from siblings.[2,3]

Kinship analysis application in forensic DNA identification is used in various cases in forensic field, for example in parentage testing (civil or criminal), disaster victim identification, missing person identification, and search of family member. Currently, paternity of the test through kinship analysis in forensic identification examination is not widely known. The objective of this study is to analyze the kinship as a technique in forensic identification.[4,5]

Methods

Population in this study was all participants who were conducted paternity test in Human Genetic Institute Tropical Disease Study Group, Universitas Airlangga. The sample of this study were from participants' peripheral blood for paternity test consisting of a father, a mother and 2 children. This study had obtained ethical eligibility from Faculty of Dentistry Universitas Airlangga No: 275/HRECC.FODM/VI/2020. There were 20 families who participated in this study with a total of 80 samples. The research was conducted in human genetic study group of Institute Tropical Disease, Airlangga University.

There were 80 peripheral blood samples that were stored in tubes and labeled as A (father), B (mother), and C (children) to refer the samples from the father, mother, and biological children.

DNA extraction process from 80 peripheral blood samples used DNAzol method (McClintock 2014). DNA pellets that were isolated were then added with 50 µl of distilled water.

DNA amplification process was through Polymerase Chain Reaction (PCR) Machine (PowerPlex® 21Systems, Promega, USA), with certain DNA sequence region target to make copies from the isolated DNA. All 80 samples were amplified using 13primer Short Tandem Repeats [STR]-Combined DNA Index System [CODIS] (TPOX, D3S1358, FGA, D5S818, CSFIPO, D7S820, D8S1179, THOI, vWA, D13S317, D16S539, D18S51, D21S11) and Amelogenin (Amel)x: 106bp, y: 112bp. Amplification setting for D3S1358, FGA, D8S1179, D18S51 ,D21S11 were as followed: 96°C-2 minutes, then [94°C-1 minute, 60°C-1 minute, 70°C-1.5 minutes, for 10 cycles), then (90°C-1 minute, 64°C-1 minute, 70°C-1.5 minutes, for 25 cycles). For CSF1PO, the setting was as followed: 96°C-2 minutes, then (94°C-1 minute, 64°C-1 minute, 70°C -1.5 minutes, for 10 cycles) then (90°C-1 minute, 64°C-1 minute, 70°C-1.5 minute, for 30 cycles). For D5S818, D7S820, D13S317 the setting was as followed: 96°C-1 minute, then [94°C-30 seconds, 60°C–30 seconds, 70°C-45 seconds, for 10 cycles), then (90°C-30 seconds, 64°C–30 seconds,70°C-45 seconds, for 30 cycles) and 60°C-30 seconds. While for D16S539 the setting was as followed: 96°C-1 minute, then (94°C-1 minute, 59°C–1 minute, 72°C-1.5 minute, for 25 cycles) and 72°C-1 minute. The DNA templates were stored at 4°C (Promega corp 2001).

Results

PCR results visualization through vertical electrophoresis with 6% polyacrylamide agarose gel [PAGE] [Bio-Rad Mini-PROTEAN®] and Silver Nitrate staining (Figure 1).

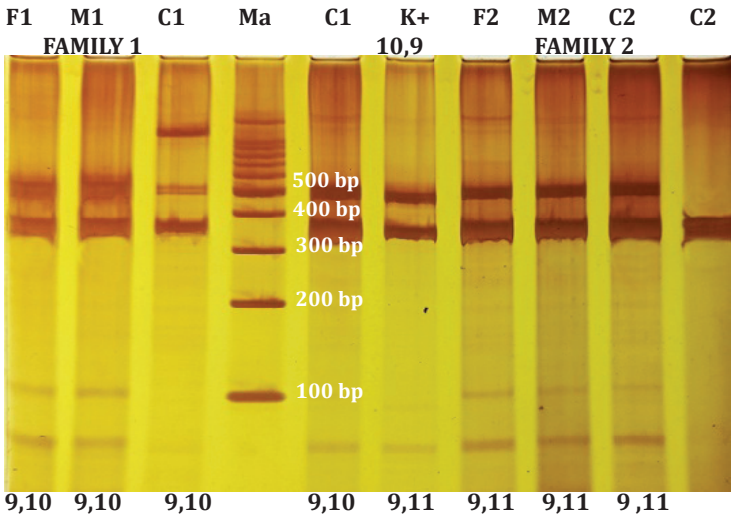

Figure 1 PCR CSF1PO locus [321bp–357bp] visualization, M [marker 100bp], A [father], B [mother], Ca [Child 1], Cb [Child 2]

DNA band contrast visualization of using locus CSF1PO establishment has responded within locus CSFIPO band limits formation (321 bp–357 bp) with Ma [100bp marker]. The sample of locus CSF1PO comes from DNA kinship paternity test from participants consisting of father, mother, and children. PCR amplification results' visualization through Polyacrylamide Agorose Gel Electrophorese (PAGE).

PCR visualization reading from electrophoresis gel in the form of alleles in each locus with K562 control (Table 1). STR Allele profile of 20 families using 13 STR CODIS TPOX, D3S1358, FGA, D5S818, CSF1PO, D7S820, D8S1179, TH01, vWA, D13S317, D16S539, D18S51, D21S11, and Amelogenin loci on 20 families consisting of father (F), mother (M), and two children (C1 and C2).

Those alleles were then matched between family members (father, mother, children) and determined their allele frequencies' value [Table 2]. STR allele frequencies on 160 samples that used 13 STR CODIS which consisted of: TPOX, D3S1358, FGA, D5S818, CSF1PO, D7S820, D8S1179, TH01, vWA, D13S317, D16S539, D18S51, D21S11, and Amelogenin loci.

Allele sharing frequencies based on kinship analysis which is between siblings in each STR CODIS (Figure 2). Allele sharing percentage on siblings using STR CODIS loci which consisted of TPOX, D3S1358, FGA, D5S818, CSF1PO, D7S820, D8S1179, TH01, vWA, D13S317, D16S539,

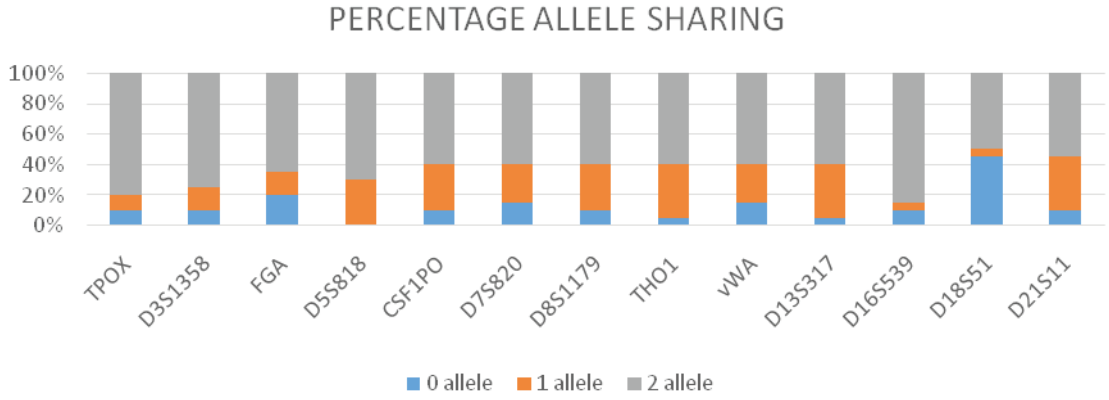

Figure 2 Allele Sharing Percentage on Siblings

Table 1 STR Allele Profile on 20 Families

		STR CODIS													
Family	**Kode**	**TPOX**	**D3S1358**	**FGA**	**D5S818**	**CSF1PO**	**D7S820**	**D8S1179**	**THO1**	**vWA**	**D13S317**	**D16S539**	**D18S51**	**D21S11**	**Amel**
1	A1	8.9	16.17	21.24	11.12	9.10	9.11	12.13	8.9	15.18	8.8	11.11	15.16	29.31	106.112
	B1	8.10	16.16	21.24	11.12	8.10	9.11	12.13	9.10	16.17	8.8	11.11	15.16	30.31	106
	C1a	8.8	16.16	21.21	12.12	8.10	9.11	12.12	9.10	15.17	8.8	11.11	15.16	30.31	106.112
	C1b	8.9	16.16	21.24	11.12	9.10	9.11	12.13	9.10	15.17	8.8	11.11	15.15	31.31	106.112
2	A2	9.10	15.17	21.22	10.12	9.10	8.8	11.12	11.13	19.20	8.9	10.11	14.15	29.31	106.112
	B2	8.9	16.17	21.24	9.10	8.9	9.10	10.11	9.10	18.19	8.10	11.13	15.15	30.31	106
	C2a	8.9	17.17	21.21	10.10	9.9	8.9	11.11	9.11	19.19	8.8	11.11	15.15	31.31	106
	C2b	8.9	15.17	21.22	10.12	8.9	8.9	11.11	9.11	19.19	8.9	11.11	15.15	31.31	106
3	A3	8.9	15.17	20.24	9.11	8.8	8.9	9.10	8.9	15.17	8.11	9.11	14.16	29.32	106.112
	B3	9.10	16.17	22.24	11.11	9.10	9.10	11.12	8.10	18.19	9.10	9.10	16.16	30.32	106
	C3a	9.10	16.17	24.24	11.11	8.9	9.9	10.11	8.8	17.18	9.11	9.9	16.16	32.32	106.112
	C3b	9.10	16.17	24.24	11.11	8.9	8.9	10.12	8.9	17.18	8.9	9.9	16.16	29.30	106.112
4	A4	9.9	16.18	22.24	8.9	9.10	8.11	9.12	11.13	20.21	9.11	10.11	15.16	31.32	106.112
	B4	9.10	17.18	21.22	10.12	9.11	9.10	12.13	11.12	16.18	9.11	10.10	16.17	29.31	106
	C4a	9.9	18.18	22.22	9.10	9.9	9.11	12.12	11.11	16.20	9.9	10.10	16.16	31.31	106.112
	C4b	9.9	18.18	21.24	9.10	9.11	8.9	12.12	11.11	16.20	9.9	10.10	16.16	31.31	106
5	A5	8.10	16.17	20.21	11.13	8.12	9.11	10.12	8.12	16.17	9.11	9.11	14.17	29.31	106.112
	B5	8.9	17.17	22.24	9.11	9.10	9.11	9.12	9.11	18.20	11.11	8.10	16.17	30.31	106
	C5a	8.8	17.17	21.22	11.11	9.12	9.9	12.12	8.9	16.18	11.11	8.9	14.16	31.31	106.112
	C5b	8.8	17.17	21.22	11.11	9.12	9.9	12.12	8.9	16.18	11.11	8.9	17.17	31.31	106
6	A6	7.10	15.18	21.21	9.11	8.9	8.10	11.12	8.9	19.20	8.9	11.13	14.15	29.31	106.112
	B6	10.11	16.17	22.23	11.11	10.11	9.11	12.13	10.13	18.19	10.12	10.12	15.15	30.31	106
	C6a	7.11	16.18	21.22	11.11	8.11	8.9	12.12	8.10	19.19	9.10	11.12	15.15	30.31	106.112
	C6b	10.11	16.18	21.23	11.11	8.11	9.10	12.12	8.10	19.19	9.10	11.12	15.15	31.31	106.112
7	A7	9.10	16.17	20.21	10.12	10.11	8.11	11.13	11.12	17.19	8.8	11.11	14.16	29.31	106.112
	B7	8.9	15.17	22.24	11.13	9.10	9.10	10.12	9.10	17.20	8.9	10.10	16.16	30.31	106
	C7a	8.9	17.17	21.22	11.12	10.10	9.11	11.12	9.11	17.17	8.8	10.11	16.16	31.31	106
	C7b	8.9	15.17	21.22	11.12	9.11	8.9	11.12	9.11	17.19	8.8	10.11	16.16	31.31	106.112
8	A8	9.10	17.19	22.24	10.12	9.11	9.11	12.13	11.12	15.17	8.9	9.11	14.17	31.32	106.112
	B8	8.9	16.18	21.23	9.11	10.11	9.11	12.13	10.11	20.21	8.10	8.10	16.17	29.31	106
	C8a	8.9	17.18	21.24	9.10	9.11	9.9	12.12	11.11	15.21	8.8	8.9	14.16	31.31	106.112
	C8b	8.9	17.18	21.24	9.10	9.11	9.9	12.13	11.11	15.21	8.9	8.9	17.17	31.31	106.112
9	A9	11.13	16.18	22.23	11.12	8.10	9.11	11.12	8.13	16.17	9.11	11.13	14.15	29.31	106.112
	B9	11.12	17.17	21.24	10.11	9.10	9.11	12.13	9.10	18.20	9.11	10.12	15.15	30.31	106
	C9a	11.11	16.17	21.24	11.11	8.9	9.9	12.12	8.9	16.18	9.9	11.12	15.15	31.31	106
	C9b	11.11	16.17	21.24	11.11	8.9	9.9	12.12	8.9	16.18	9.9	11.12	15.15	31.31	106.112
10	A10	10.11	15.17	20.24	9.11	8.12	9.11	11.13	8.11	15.18	9.11	10.11	15.16	31.32	106.112
	B10	9.10	16.18	19.22	11.13	8.10	11.11	10.12	8.9	16.17	11.11	10.10	16.17	29.31	106
	C10a	10.10	15.18	20.22	11.11	8.8	11.11	11.12	8.8	15.17	11.11	10.10	16.16	31.31	106.112
	C10b	9.11	16.17	20.22	9.13	8.8	11.11	11.12	8.8	15.17	11.11	10.10	16.16	31.31	106.112
11	A11	11.13	15.17	19.21	10.12	9.10	8.8	12.13	8.9	15.17	9.11	9.11	14.17	29.31	106.112
	B11	11.12	16.18	21.23	9.11	9.11	8.8	12.13	10.13	18.19	11.11	8.10	16.17	30.31	106
	C11a	11.11	15.18	21.21	9.10	9.9	8.8	12.12	8.10	17.18	11.11	8.9	14.16	31.31	106.112
	C11b	11.11	16.17	21.21	9.10	9.11	8.8	12.13	8.10	17.18	11.11	8.9	17.17	31.31	106.112

Table 1 STR Allele Profile on 20 Families

		STR CODIS													
Family	**Kode**	**TPOX**	**D3S1358**	**FGA**	**D5S818**	**CSF1PO**	**D7S820**	**D8S1179**	**THO1**	**vWA**	**D13S317**	**D16S539**	**D18S51**	**D21S11**	**Amel**
12	A12	11.13	16.17	20.24	10.12	9.11	8.9	12.13	11.12	20.21	8.8	11.13	14.15	29.31	106.112
	B12	11.12	16.16	19.22	9.11	10.11	8.10	12.13	9.10	16.18	8.8	10.12	15.15	30.31	106
	C12a	11.11	16.16	20.22	9.10	9.11	8.8	12.12	9.11	16.20	8.8	11.12	15.15	30.31	106
	C12b	11.11	16.16	20.22	9.10	9.11	8.9	12.13	9.11	16.20	8.8	11.12	15.15	31.31	106
13	A13	9.10	16.17	22.24	10.12	8.10	8.11	11.12	8.13	15.18	8.9	10.11	15.16	29.31	106.112
	B13	8.9	17.17	21.23	9.10	9.10	9.10	12.13	9.10	16.17	8.10	10.10	16.17	30.31	106
	C13a	8.9	17.17	21.24	10.10	8.9	9.11	12.12	8.9	15.17	8.8	10.10	16.16	31.31	106.112
	C13b	8.9	17.17	21.24	10.12	8.9	8.9	12.12	8.9	15.17	8.9	10.10	16.16	31.31	106.112
14	A14	8.9	15.18	22.23	9.11	8.12	9.11	11.13	8.11	16.17	8.8	9.11	14.17	29.31	106.112
	B14	9.10	16.17	21.24	11.11	8.10	9.11	10.12	8.9	18.20	8.8	8.10	16.17	30.31	106
	C14a	9.10	16.18	21.24	11.11	8.8	9.9	11.12	8.8	16.18	8.8	8.9	14.16	30.31	106.112
	C14b	9.10	16.18	21.24	11.11	8.8	9.9	11.12	8.8	16.18	8.8	8.9	17.17	31.31	106
15	A15	9.9	17.19	21.24	8.9	9.10	9.11	12.13	11.13	15.18	9.11	9.11	14.17	28.30	106.112
	B15	9.10	16.18	21.24	10.12	9.11	11.11	12.13	11.12	16.17	9.11	8.10	16.17	30.31	106
	C15a	9.9	17.18	21.21	9.10	9.9	11.11	12.12	11.11	15.17	9.9	8.9	14.16	30.30	106.112
	C15b	9.9	17.18	21.24	9.10	9.11	11.11	12.13	11.11	15.17	9.9	8.9	17.17	30.31	106
16	A16	9.10	16.18	21.22	8.9	8.12	8.9	11.12	8.12	19.20	9.11	10.11	15.16	31.32	106.112
	B16	8.9	17.17	21.24	10.12	8.10	8.10	10.11	9.11	18.19	11.11	10.10	16.17	29.31	106
	C16a	8.9	16.17	21.21	9.10	8.8	8.8	11.11	8.9	19.19	11.11	10.10	16.16	31.31	106.112
	C16b	8.9	16.17	21.22	9.10	8.8	8.9	11.11	8.9	19.19	11.11	10.10	16.16	31.31	106.112
17	A17	11.13	15.17	20.24	10.12	9.10	9.11	9.10	11.13	17.19	8.8	9.11	14.17	29.31	106.112
	B17	11.12	16.18	19.22	9.10	9.11	9.11	11.12	9.10	17.20	8.8	8.10	16.17	30.31	106
	C17a	11.11	15.18	20.22	10.10	9.9	9.9	10.11	9.11	17.17	8.8	8.9	14.16	31.31	106
	C17b	11.11	16.17	20.22	10.12	9.11	9.9	10.12	9.11	17.19	8.8	8.9	17.17	31.31	106.112
18	A18	10.11	16.17	22.24	8.9	8.12	9.11	11.13	8.9	16.17	8.9	11.13	14.15	29.31	106.112
	B18	9.10	16.16	21.23	10.12	9.10	11.11	10.12	9.10	18.20	8.10	10.12	15.15	30.31	106
	C18a	10.10	16.16	21.24	9.10	9.12	11.11	11.12	9.10	16.18	8.8	11.12	15.15	30.31	106.112
	C18b	9.11	16.16	21.24	9.10	9.12	11.11	11.12	9.10	16.18	8.9	11.12	15.15	31.31	106.112
19	A19	11.13	15.18	21.24	9.11	8.12	9.11	12.13	11.13	19.20	8.11	9.11	14.17	31.32	106.112
	B19	11.12	16.17	21.24	11.13	8.10	11.11	12.13	9.10	18.19	9.10	8.10	16.17	29.31	106
	C19a	11.11	16.18	21.21	11.11	8.8	11.11	12.12	9.11	19.19	9.11	8.9	14.16	31.31	106
	C19b	11.11	16.18	21.24	9.13	8.8	11.11	12.13	9.11	19.19	8.9	8.9	17.17	31.31	106.112
20	A20	9.9	17.19	21.22	10.12	9.10	8.8	11.12	8.13	17.19	8.9	11.13	14.15	29.31	106.112
	B20	9.10	16.18	21.24	9.11	9.11	8.8	10.11	9.10	17.20	8.10	10.12	15.15	30.31	106
	C20a	9.9	17.18	21.21	9.10	9.9	8.8	11.11	8.9	17.17	8.8	11.12	15.15	31.31	106.112
	C20b	9.9	17.18	21.22	9.10	9.11	8.8	11.11	8.9	17.19	8.8	11.12	15.15	31.31	106.112

Table 2 Allele STR Frequencies of Samples (n=160)

Allele	Frequency	Allele	Frequency
TPOX		THOI	
7	0.013	8	0.25250
8	0.175	9	0.27000
9	0.3437	10	0.10750
10	0.18125	11	0.27000
11	0.22500	12	0.05000
12	0.03125	13	0.05000
13	0.03125		
D3S1358		vWA	
15	0.09375	15	0.12750
16	0.33125	16	0.10750
17	0.35000	17	0.19500
18	0.20625	18	0.22250
19	0.01875	19	0.19500
		20	0.10250
		21	0.05000
FGA		D13S317	
19	0.03750	8	0.43750
20	0.08750	9	0.25625
21	0.35625	10	0.06250
22	0.22500	11	0.23750
23	0.05000	12	0.00625
24	0.24375		
D5S818		D16S539	
8	0.02500	8	0.13125
9	0.21250	9	0.16875
10	0.25625	10	0.29375
11	0.32500	11	0.28125
12	0.14375	12	0.08750
13	0.03750	13	0.03750
CSF1PO		D18S51	
8	0.23250	14	0.13750
9	0.35750	15	0.31875
10	0.20250	16	0.34375
11	0.15750	17	0.20000
12	0.05000		
D8S1179		D21S11	
9	0.02500	28	0.00625
10	0.08750	29	0.12500
11	0.23125	30	0.16875
12	0.50000	31	0.64375
13	0.15625	32	0.05625
D7S820			
8	0.25000		
9	0.38125		
10	0.05625		
11	0.3125		

D18S51, D21S11, and Amelogenin loci with blue color which represents 0 allele sharing, red color represents 1 allele sharing, and black represents 2 allele sharing.

Discussion

DNA sample extraction results were measured their level and purity, with mean DNA sample level of 675±5.35ng/µL while DNA purity ranged from 1.05 – 1.86. Furthermore, PCR amplification through 13 STR-CODIS loci primers as well as PCR results visualization through polyacrylamide agarose gel electrophorese (PAGE) with silver nitrate staining, including the PCR visualization results, were as followed:

Individual genetic material is obtained from

both parents by 50% each. Since a person's nuclear DNA is inherited from the father and mother, it is said that nuclear DNA [nDNA] is inherited in a Mendellian manner. In Mendel's law 1 (segregation of allelic genes) stated the rules of allele separation at the time of gamete formation. Gamete formation occurs by meiosis, where homologous pairs separate from each other and do not pair again/there is a free separation of gene alleles from diploid to haploid.[6,7,8]

In genetics, alleles are alternative forms of genes at a locus in correlation to trait expression (phenotype). Alleles are formed due to nitrogen base sequence variations because of mutations. In an individual, allele pairs determine the individual genotype. The term allele arises from the use of allelomorphs in Mendel's Principles of Heredity.[4,8,9]

Individuals who have the same allele at a locus are said to have homozygous genotypes, while those who have different alleles are said to be heterozygous. Because genotype is expressed as a phenotype, alleles might cause differences in appearance among individuals in a population.[4,5]

Paternity test is a DNA test to determine whether a man is the biological father of a child. Cases of family disputes, for example when the parents are doubted, doubts about fathers and mothers, are cases that are increasingly found in Indonesian society.[3]

Parents are the comparison in paternity test, where the obtained results are statistically near to 100% or around 99.99%.[10] Unavailable information from the parents or the child that can be used as comparisons in forensic DNA examination process is one of the problems that might occur in forensic DNA analysis.[1] Unlike DNA testing that uses the parent's DNA as comparisons, individual identification using siblings' DNA has an accuracy rate that is not near to 100%.[11]

The results of our study regarding STR CODIS loci alleles on paternity test in Human Genetic Study group ITD Universitas Airlangga, the highest percentage of locus alleles were: TPOX allele 9 (34.375%), D3S1358 allele 17 [35%], FGA allele 21 (35.62%), D5S818 allele 11 (32.5%), CSF1PO allele 9 (35.75%), DS820 allele 9 (38.12%), D8S1179 allele 12 (50%), THOI allele 9 (27%), vWA allele 18 (22.25%), D13S317 allele 8 (43.75%), D16S539 allele 10 (29.38%), D18S51 allele 16 (34.38%) and D21S11 allele 31 (64.38%)(Table 2).

The principle of identification through DNA is based on allele comparison process between alleles from the victims or perpetrators with alleles from the family line, especially parents according to Mendel's law.[12,13,14] However, if parental or biological children line are not available, a comparison is needed from close family line as one of the methods that can be considered in identification through DNA, such as from siblings. The use of sibling as a comparison is one of identification methods, which is known as kinship analysis. Kinship analysis in identification process using siblings as a comparison, as in paternity test, will meet a possibility of mismatch in DNA locus profile that is used.[7,11,14,15]

In kinship analysis, allele sharing plays an important role. Allele sharing in determining siblings is very useful in establishing the relationship between the siblings when both alleles are involved. Statistically, full siblings have a 2 alleles accuracy of (0.25) 25%, this value is the same as not having the same allele or 0 allele, while the accuracy of 1 allele reaches 50%.[11]

The result of this study differed from a theory presented by O'Connor where all CODIS STR loci that were examined showed that allele sharing was dominated by 2 allele sharing.[11] This is because the data that were conducted with paternity test were not only on certain races or ethnicities, but almost all races or ethnicities who were conducted with paternity test in the Human Genetic ITD study group, Airlangga University. Marker is needed in personal identification of forensic DNA, especially in paternity test, to answer the doubts of a forensic DNA expert in drawing conclusions, which is through mitochondrial DNA (mtDNA) and Y chromosome (Y-STRs) examinations as available alternatives.[4]

Allele sharing is a genetic variation inherited from both parents. All individuals are part of the population as a result of mating between individuals and have the same gene pool. Gene pool is a collection of all genes/alleles in the population.[7] Hardy-Weinberg Equilibrium Principle emphasizes that in a population that is in equilibrium, genes and genotypes frequencies will remain from one generation to the next. This is found in large populations, marriages that take place randomly, and no attempt to regulate certain traits.[8]

Paternity test is based on allele comparison process from both parents. If there is no comparison from the parents, comparison comes from the closest family/kinship line, especially from parental line according to Mendel law. One of these kinship lines are from siblings.

When assessing full sibling relationships, careful consideration must be taken of the high frequency STR loci at 2 allele shares. The results of this study were all CODIS STR loci had the highest percentage of 2 allele sharing, therefore it is recommended that paternity test might be conducted through sibling or kinship pathways [Kinship] if both parents are not present.

The conclusion of this study is forensic identification using kinship analysis can be done using STR-CODIS locus, but there are some distinction in the percentage and qualification of using these locus. The main reason of forensic identification using kinship analysis is based on the mendelian law which state the gen of the parents will be inherited in to their generations. So, it is useful to identify the person using his sibling DNA when DNA from their parents is absent.

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